

73
SEQUENCE LISTING

(1)

GENERAL INFORMATION:

- (i) APPLICANT: Yoram Reiter
- (ii) TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-
COMPATIBILITY COMPLEXES, CONSTRUCTS
ENCODING SAME AND METHODS OF GENERATING
SAME
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE:
- (B) STREET:
- (C) CITY:
- (D) STATE:
- (E) COUNTRY:
- (F) ZIP:
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME:
- (B) REGISTRATION NUMBER:
- (C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE:
- (B) TELEFAX:
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Met Asp Gln Val Pro Phe Ser Val

5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Leu Glu Pro Gly Pro Val Thr Val

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Leu Phe Gly Tyr Pro Val Tyr Val

5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1248
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGATCCAGC GTACTCCAAA GATTGAGTT TACTCACGTC ATCCAGCAGA 50
 GAATGGAAAG TCAATTTCC TGAATTGCTA TGTGTCTGGG TTTCATCCAT 100
 CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG 150
 GAGCATTCAG ACTTGTCTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA 200
 TTATACTGAG TTCACCCCCA CTGAAAAAGA TGAGTATGCC TGCCGTGTGA 250

ACCACGTGAC TTTGTCACAG CCAAGATAG TTAAGTGGGA TCGAGACATG 300
 GGTGGCGGTG GAAGCGGCGG TGGAGGCTCT GGTGGAGGTG GCAGCGGCTC 350
 TCACTCCATG AGGTATTTCT TCAATCCGT GTCCCGGCCC GGCCGCGGGG 400
 AGCCCCGCTT CATCGCAGTG GGCTACGTGG ACGACACGCA GTTCGTGCGG 450
 TTGCACAGCG ACGCCGCGAG CCAGAGGATG GAGCCGCGGG CGCCGTGGAT 500
 AGAGCAGGAG GGTCCGGAGT ATTGGGACGG GGAGACACGG AAAGTGAAGG 550
 CCCACTCACA GACTCACCGA GTGGACCTGG GGACCCTGCG CGGCTACTAC 600
 AACCAGAGCG AGGCCGGTTC TCACACCGTC CAGAGGATGT ATGGCTGCGA 650
 CGTGGGGTCG GACTGGCGCT TCCTCCGCGG GTACCACCAG TACGCCTACG 700
 ACGGCAAGGA TTACATCGCC CTGAAAGAGG ACCTGCGCTC TTGGACCGCG 750
 GCGGACATGG CAGCTCAGAC CACCAAGCAC AAGTGGGAGG CGGCCCATGT 800
 GCGGAGCAG TTGAGAGCCT ACCTGGAGGG CACGTGCGTG GAGTGGCTCC 850
 GCAGATACCT GGAGAACGGG AAGGAGACGC TGCAGCGCAC GGACGCCCCC 900
 AAAACGCACA TGA CTCACCA CGCTGTCTCT GACCATGAAG CCACCCTGAG 950
 GTGCTGGGCC CTGAGCTTCT ACCCTGCGGA GATC CACTG ACCTGGCAGC 1000
 GGACTTGGAG GAATCTTTGA GGCAATGAAG ATGGAGCTGC GGGACTGA 1248

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro
 5 10 15
 Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly
 20 25 30
 Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
 35 40 45
 Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp
 50 55 60
 Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu
 65 70 75
 Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln
 80 85 90
 Pro Lys Ile Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
 95 100 105
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser His Ser Met
 110 115 120

Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro		
125	130	135
Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg		
140	145	150
Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro		
155	160	165
Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr Arg		
170	175	180
Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr		
185	190	195
Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val		
200	205	210
Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu		
215	220	225
Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala		
230	235	240
Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala		
245	250	255
Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln		
260	265	270
Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg		
275	280	285
Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro		
290	295	300
Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr		
305	310	315
Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu		
320	325	330
Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu		
335	340	345
Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala		
350	355	360
Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His		
365	370	375
Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu		
380	385	390
Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly Gly Leu Gly Gly Ile		
395	400	405
Phe Glu Ala Met Lys Met Glu Leu Arg Asp		
410	415	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro
 5 10 15
 Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp
 20 25 30
 Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met
 35 40 45
 Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp
 50 55 60
 Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg
 65 70 75
 Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala
 80 85 90
 Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser
 95 100 105
 Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly
 110 115 120
 Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala
 125 130 135
 Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala
 140 145 150
 His Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val
 155 160 165
 Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln
 170 175 180
 Arg Thr Asp Ala Pro Lys Thr His Met Thr His His Ala Val Ser
 185 190 195
 Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro
 200 205 210
 Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr
 215 220 225
 Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
 230 235 240
 Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln

245 250 265
 Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu
 270 275 280
 Thr Leu Arg Trp Glu Gln Ser Thr Arg Gly
 285 290

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro
 5 10 15
 Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly
 20 25 30
 Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
 35 40 45
 Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp
 50 55 60
 Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu
 65 70 75
 Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln
 80 85 90
 Pro Lys Ile Val Lys Trp Asp Arg Asp Met
 95 100

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGAGATATA CATATGGGCT CTCCTCCAT GAGGTA 36

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCTTTGT TAGCACCGAT TCATAGGTGA GGGGCTTGGG CAA 43

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGATATAC ATATGATCCA GCGTACTCCA AAGAT 35

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGGCTTTGT TAGCAGCCGA ATTCATTACA TGTCTCGATC CCACTTAAC 49

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAAGGCGTT GGCGCATATG ATCCAGCGTA CTCCAAGAT T 41

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAAGCGGCG GTGGAGGCTC TGGTGGAGGT GGCAGCGGCT CTCACTCCAT 50
GA 52

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGCGGCG GTGGAGGCTC TGGTGGAGGT GGCAGCGGCT CTCACTCCAT 50
GA 52

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGAGAATTC TTACTCCCAT CTCAGGGTGA GGGGCTTGGG CAA 43

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp

5

10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly Gly

5

10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGTAAAAGC TTTTATCAG CCTCCGAACT GTGGATGCCT CCACGCCGAA 50

CCTCCACCAG AACCACCTCC GGACCCGCCA CCTCCCTCCC ATCTCAGGGT 100

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATCTTTG AGGCAATGAA GATGGAGCTG CGGGACTGA 39